JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST - 3 EXAMINATION - MAY-2023

COURSE CODE(CREDITS): 18B1WBI831 (3)   MAX. MARKS: 35

COURSE NAME: Computational Molecular Evolution

COURSE INSTRUCTORS: Dr. Tiratha Raj Singh   MAX. TIME: 2 Hours

Note: All questions are compulsory. Marks are indicated against each question in square brackets.

Q.1. Derive two parameter model for the evolution of DNA sequences. Justify that this model can recover the deficiencies proposed in the one parameter model of Jukes and Cantor. Explain the major differences between these two models for the nucleotide substitutions.   (CO:1-4) [6]

Q.2. Discuss in an elaborative way, the process of evolution at molecular level. Explain how human is having only once current species? Are we still evolving? Justify your answer with some proofs available currently in any form.   (CO:1-3) [4]

Q.3. Make a derivation of non-functionalization time for a set of genes. Consider the involvement of two species while gene duplication happened in one of these species. Duplicated gene got non-functionalized after an amount of time. T_D (gene duplication time), T_N (gene non-functionalization time). Total time of divergence is T.   (CO:4,5) [6]

Q.4. What is phylogeny? What are various methods used for the analysis of phylogeny through molecular sequences? Discuss the method of estimating branch lengths for phylogenetic tree with an example with 5 nodes and 7 branches. Assume the weights on branches as per the length of these branches.   (CO:4, 5) [5]

Q.5. What is codon usage bias (CUB)? Discuss any 5 measures of codon usage with a major emphasis on Codon adaptive index.   (CO:3, 4) [4]

Q.6. Elaborate about the two major evolution theories for the introns. Provide a comparative view of these theories for the evolution of introns. Discuss the functional role of introns in the process of genomic regulations.   (CO:4, 5) [4]

Q.7. Explain following terms *w.r.t.* evolution: (CO:1-5) [1.5*4=6]

(a) Basic Mathematical Model   (b) Gene expression and codon usage

(c) Gene duplication and dating   (d) Genome evolution